

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 30, 2002, 12:02:18 ; Search time 16.7346 Seconds

(without alignments)
2282.679 Million cell updates/sec

File: US-10-054-680-2

Sequence: 1 MAMLRQPLRSALFLHGLVT.....LWLLYLFATLLEACVYIKGF 921

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt.40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4686	97.7	927	NAC3_RAT	P70549 rattus norv
2	3447.5	71.9	970	NAC1_CANFA	P23685 canis famli
3	3442.5	71.8	970	NAC1_FELCA	P48767 felis silve
4	3439.5	71.7	973	NAC1_HUMAN	P32418 homo sapien
5	3432.5	71.6	970	NAC1_CANVO	P48766 cavia porce
6	3428	71.5	971	NAC1_RAT	P01728 rattus norv
7	3425.5	71.4	970	NAC1_BOVIN	P48765 bos taurus
8	3405.5	71.0	970	NAC1_MOUSE	P70414 mus musculu
9	3373.5	70.3	921	NAC2_HUMAN	O94915 homo sapien
10	3357	70.0	921	NAC2_RAT	P48768 rattus norv
11	3093	64.5	595	NAC3_HUMAN	P57103 homo sapien
12	306.5	6.4	1216	NKX1_BOVIN	O28139 bos taurus
13	303.5	6.3	1181	NKX1_RAT	O28139 rattus norv
14	293	6.1	1099	NKX1_HUMAN	O60721 homo sapien
15	266	5.5	645	NKX3_MOUSE	O99397 mus musculu
16	262.5	5.5	624	NKX3_RAT	O99390 rattus norv
17	258.5	5.4	644	NKX3_HUMAN	O99358 homo sapien
18	251	5.2	663	NKX1_CHICK	O91418 gallus gall
19	239.5	5.0	661	NKX2_HUMAN	O91410 homo sapien
20	231.5	4.8	856	NCKX_DROME	O94640 drosophila
21	227	4.7	670	NKX2_RAT	O54701 rattus norv
22	216.5	4.5	651	NKX2_CHICK	O91417 gallus gall
23	147	3.1	590	YRTA_CAEL	P43322 caenorhabdi
24	143.5	3.0	325	YRTB_ECOLI	P43324 caenorhabdi
25	142.5	3.0	1807	YRTB_ECOLI	O64632 rattus norv
26	142	3.0	302	Y091_METU	O57556 methanococc
27	141.5	2.9	572	YRT4_CAEL	P34315 caenorhabdi
28	138.5	2.7	664	SYM_BACST	P34365 bacillus su
29	128.5	2.7	4655	LRP2_HUMAN	P98164 homo sapien
30	127	2.6	1822	ITB4_HUMAN	P16144 homo sapien
31	125	2.6	700	TRDN_CANFA	P82179 canis famli
32	120	2.5	1828	MAP2_MOUSE	P20357 mus musculu
33	119.5	2.5	1564	MRP2_RABIT	O28689 oryctolagus

34	118	2.5	803	1	RIR1_CRYPV	O61065 cryptospori
35	115.5	2.4	1805	1	NES1_RAT	P21263 rattus norv
36	115	2.4	548	1	CH60_EHRE	O32606 ehrlichia s
37	114	2.4	1036	1	YAN2_SCHPO	Q10068 schizosacch
38	114	2.4	1468	1	RPOB_AOUAE	O67762 aquilex aeo
39	113.5	2.4	548	1	CH60_EHRE	P48214 ehrlichia r
40	113.5	2.4	661	1	Y102_MYCTU	Q10897 mycobacteri
41	113.5	2.4	1332	1	SPT7_YEAST	P35177 saccharomyc
42	113.5	2.4	1612	1	ATC4_YEAST	Q12675 saccharomyc
43	112	2.3	853	1	YCG1_YEAST	P25588 saccharomyc
44	112	2.3	1112	1	RA13_SCHPO	P28706 schizosacch
45	111.5	2.3	853	1	WMT4_LAMBD	P03736 bacterioph

ALIGNMENTS

RESULT 1	ID	NAME	STANDARD	PRT	927 AA
NAC3_RAT	AC	P70549			
DT	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein 3).				
GN	SLC8A3 OR NCX3.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RM	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;				
RX	MEDLINE=96394663; PubMed=8798769;				
RA	Nicola D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,				
RA	Phillipson K.D.;				
RT	"Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.,"				
RL	J. Biol. Chem. 271:24914-24921(1996).				
CC	-1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION				
CC	COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION				
CC	SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.				
CC	-1- ENZYME REGULATION: BY INTRACELLULAR CALCIUM IONS.				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
CC	-1- TISSUE SPECIFICITY: EXPRESSION RESTRICTED TO BRAIN AND SKELETAL				
CC	MUSCLE.				
CC	-----				
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CC	-----				
CC	EMBL: U53420; AAC52817.1; -				
DR	InterPro: IPR003644; Calx_beta.				
DR	InterPro: IPR004837; NaCa_Exmemb.				
DR	InterPro: IPR004836; NaCa_Ex.				
DR	Pfam: PF01699; Na_Ca_Ex. 2.				
DR	Pfam: PF03160; Calx_beta. 2.				
DR	PRINTS: PR01259; NACAEXCHNGR.				
DR	SMART: SM00237; Calx_beta. 2.				
DR	TIGRFAMS: TIGR00845; caca; 1.				
KW	Transmembrane; Glycoprotein; Phosphorylation; Signal;				
KW	Transmembrane; Glycoprotein; Phosphorylation; Signal;				
KW	Calmodulin-binding; Repeat.				
FT	SIGNAL	1	30		POTENTIAL.
FT	CHAIN	1	927		SODIUM/CALCIUM EXCHANGER 3.
FT	DOMAIN	31	73		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	74	94		POTENTIAL.
FT	DOMAIN	95	147		CYTOSOLIC (POTENTIAL).
FT	TRANSMEM	148	168		POTENTIAL.

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FT DOMAIN 169 169 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 170 190 POTENTIAL.
FT DOMAIN 191 202 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 203 223 POTENTIAL.
FT DOMAIN 224 230 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 231 251 POTENTIAL.
FT DOMAIN 252 276 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 277 276 POTENTIAL.
FT TRANSMEM 748 754 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 755 775 POTENTIAL.
FT DOMAIN 776 778 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 779 799 POTENTIAL.
FT DOMAIN 800 828 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 829 849 POTENTIAL.
FT TRANSMEM 850 860 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 861 881 POTENTIAL.
FT DOMAIN 882 903 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 904 924 POTENTIAL.
FT DOMAIN 925 927 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 253 272 CALMODULIN-BINDING (BY SIMILARITY).
FT REPEAT 140 180 ALPHA-1.
FT REPEAT 399 470 BETA-1.
FT REPEAT 534 604 BETA-2.
FT REPEAT 796 832 ALPHA-2.
FT DOMAIN 645 648 POLY-GLU.
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 823 823 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 927 AA; 103162 MW; EAB35F9620DBE69E CRC64;

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Query Match 97.7%; Score 4686; DB 1; Length 927;

Best Local Similarity 96.8%; Pred. No. 1.6e-300;

Matches 897; Conservative 14; Mismatches 10; Indels 6; Gaps 1;

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OY 1 MAWLRLQPLTSALFHGGLVFLVFLNGLRAGSGSDVPSTGNNESCSSSPCKRECVIL 60
DB 1 MAWLRLQPLTSALFHGGLVFLVFLNGLRAGSDLDVPSAGNNESCSSSPCKRECVIL 60
OY 61 PIWYRPNPISGDKIARIYVYFVALIYMWLGVSIIADRFNASIEVITSQEREVITIKRNGE 120
DB 61 PIWYRPNPISGDKIARIYVYFVALIYMWLGVSIIADRFNASIEVITSQEREVITIKRNGE 120
OY 121 TSTTTIRVWNETVSNLTLMALGSSAPRILLSLIEVCGHGFIADLPSTIVGSAAFMFI 180
DB 121 TSTTTIRVWNETVSNLTLMALGSSAPRILLSLIEVCGHGFIADLPSTIVGSAAFMFI 180
OY 181 IIGICVIVIDGERTKIKHLRVEFTIAMSIFRYIMLYMLAVFSPVVOVWEGLLTLFF 240
DB 181 IIGICVIVIDGERTKIKHLRVEFTIAMSIFRYIMLYMLAVFSPVVOVWEGLLTLFF 240
OY 241 FVYCVLLAWADRLRLFYKYMKRKYRTDKHGGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
DB 241 FVYCVLLAWADRLRLFYKYMKRKYRTDKHGGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
OY 301 LVPLEGEVDESREMRIRIKDKOKHPEKDLDQVEMANYALSHOOKRAATYRIQATR 360
DB 301 LVPLEGEVDESREMRIRIKDKOKHPEKDLDQVEMANYALSHOOKRAATYRIQATR 360
OY 361 MMTGAGNIIKKHAEOKKASMSSEVHTDEPEDFISVFEPDPSYOCLEMGAVLLTVR 420
DB 361 MMTGAGNIIKKHAEOKKASMSSEVHTDEPEDFISVFEPDPSYOCLEMGAVLLTVR 420
OY 421 KGGDSKTMVVDYKTEDEGSANAGADYEFTGTVVLKPGETOKESVGIIDDDI FEEDENF 480
DB 421 KGGDSKTMVVDYKTEDEGSANAGADYEFTGTVVLKPGETOKESVGIIDDDI FEEDENF 480
OY 481 FVRLSNRRIEEOPEECPAIFNSLPLPRAVLASPCVAVATVITLDDHAGIFFECDTH 540
DB 481 FVRLSNRRIEEOPEECPAIFNSLPLPRAVLASPCVAVATVITLDDHAGIFFECDTH 540
OY 541 VSESIGMEVKVLRTSARGTVIYVPTVEGTAKGGGEDEEDYIGELFEFNDETIVKIRV 600
DB 541 VSESIGMEVKVLRTSARGTVIYVPTVEGTAKGGGEDEEDYIGELFEFNDETIVKIRV 600

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OY 601 KIVDEEYERQENFTALGEPKMERGIS-----DYTRKLTMEBEAKRIAEKGPVL 654
DB 601 KIVDEEYERQENFTALGEPKMERGIS-----DYTRKLTMEBEAKRIAEKGPVL 660
OY 655 GEHPKLEVIIEESYERKTVNDKIKRTNLALVYGTSHWBDQFEATVTSAGDEDESG 714
DB 661 GEHPKLEVIIEESYERKTVNDKIKRTNLALVYGTSHWBDQFEATVTSAGDEDESG 720
OY 715 EERLPSCFDVYVHFLTFVFKVLEFACVPPTREYCHGACFAVSIIIGMLTAIIGDLASHRG 774
DB 721 EERLPSCFDVYVHFLTFVFKVLEFACVPPTREYCHGACFAVSIIIGMLTAIIGDLASHRG 780
OY 775 CTIGLKDSTAVYVFAFGISVPTPFSKAAALODYADASIGVNTSSNAVNFILGIGLAW 834
DB 781 CTIGLKDSTAVYVFAFGISVPTPFSKAAALODYADASIGVNTSSNAVNFILGIGLAW 840
OY 835 SVATITWALOGGEFHVSAGTLAFSVTLFTFAFVCSIVLLYRRRPHLGGELGPRCKKLA 894
DB 841 SVATITWALOGGEFHVSAGTLAFSVTLFTFAFVCSIVLLYRRRPHLGGELGPRCKKLA 900
OY 895 TTVLFWSLMILYILFATLEAYCIYKGF 921
DB 901 TTVLFWSLMILYILFATLEAYCIYKGF 927

RESULT 2
ID NACL_CANFA STANDARD; PRT; 970 AA.
AC P23685;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
  1).
GN SLC8A1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RA MEDLINE=91047958; PubMed=1700476;
RA NCIID D.A., Longoni S., Philipson K.D.;
RT "Molecular cloning and functional expression of the cardiac
  sarcolemmal Na(+)-Ca2+ exchanger.";
RL Science 250:562-565(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Heart;
RX MEDLINE=92152737; PubMed=1785844;
RA NCIID D.A., Philipson K.D.;
RT "Molecular studies of the cardiac sarcolemmal sodium-calcium
  exchanger.";
RL Ann. N.Y. Acad. Sci. 639:181-188(1991).
CC COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
  SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION. BY ATP.
CC -1- SUBCELLULAR LOCATION. Integral membrane protein. Plasma membrane.
CC -1- TISSUE SPECIFICITY. CARDIAC SARCOLEMA.
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DR EMBL: M57523; AAA62766.1; -
DR PIR: A36417; A36417.
DR InterPro: IPR003644; Calx_beta.

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DR InterPro: IPR004837; NaCa_Exmemb.
 DR InterPro: IPR004836; Na_Ca_Ex.
 DR Pfam: PF01699; Na_Ca_Ex. 2.
 DR Pfam: PF03160; Calx_beta; 2.
 DR PRINTS: PR01259; NACAEXCHNGR.
 DR SMART: SM00237; Calx_beta; 2.
 DR TIGRFAMs: TIGR00845; caca; 1.
 KW Transport: Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOSOLSMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOSOLSMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 POTENTIAL.
 FT DOMAIN 250 269 CYTOSOLSMIC (POTENTIAL).
 FT TRANSMEM 270 789 POTENTIAL.
 FT DOMAIN 790 796 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 797 819 POTENTIAL.
 FT DOMAIN 820 821 CYTOSOLSMIC (POTENTIAL).
 FT TRANSMEM 822 840 POTENTIAL.
 FT DOMAIN 841 871 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 872 892 POTENTIAL.
 FT DOMAIN 893 903 CYTOSOLSMIC (POTENTIAL).
 FT TRANSMEM 904 924 POTENTIAL.
 FT DOMAIN 925 941 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 942 958 POTENTIAL.
 FT DOMAIN 959 970 CYTOSOLSMIC (POTENTIAL).
 FT TRANSMEM 971 976 CALMODULIN-BINDING (POTENTIAL).
 FT DOMAIN 977 1004 ALPHA-1.
 FT TRANSMEM 1005 1018 BETA-1.
 FT DOMAIN 1019 1032 BETA-2.
 FT TRANSMEM 1033 1046 ALPHA-2.
 FT DOMAIN 1047 1060 POLY-PHE.
 FT TRANSMEM 1061 1074 POLY-GLU.
 FT DOMAIN 1075 1088 POLY-ASP.
 FT TRANSMEM 1089 1102 PHOSPHORYLATION (POTENTIAL).
 FT DOMAIN 1103 1116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT TRANSMEM 1117 1130 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DOMAIN 1131 1144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT TRANSMEM 1145 1158 CARBOHYD.
 FT DOMAIN 1159 1172 CARBOHYD.
 FT TRANSMEM 1173 1186 CARBOHYD.
 FT DOMAIN 1187 1200 CARBOHYD.
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 FT DOMAIN 1215 1228 CARBOHYD.
 FT TRANSMEM 1229 1242 CARBOHYD.
 FT DOMAIN 1243 1256 CARBOHYD.
 FT TRANSMEM 1257 1270 CARBOHYD.
 FT DOMAIN 1271 1284 CARBOHYD.
 FT TRANSMEM 1285 1298 CARBOHYD.
 FT DOMAIN 1299 1312 CARBOHYD.
 FT TRANSMEM 1313 1326 CARBOHYD.
 FT DOMAIN 1327 1340 CARBOHYD.
 FT TRANSMEM 1341 1354 CARBOHYD.
 FT DOMAIN 1355 1368 CARBOHYD.
 FT TRANSMEM 1369 1382 CARBOHYD.
 FT DOMAIN 1383 1396 CARBOHYD.
 FT TRANSMEM 1397 1410 CARBOHYD.
 FT DOMAIN 1411 1424 CARBOHYD.
 FT TRANSMEM 1425 1438 CARBOHYD.
 FT DOMAIN 1439 1452 CARBOHYD.
 FT TRANSMEM 1453 1466 CARBOHYD.
 FT DOMAIN 1467 1480 CARBOHYD.
 FT TRANSMEM 1481 1494 CARBOHYD.
 FT DOMAIN 1495 1508 CARBOHYD.
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 FT DOMAIN 1859 1872 CARBOHYD.
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 FT TRANSMEM 2461 2474 CARBOHYD.
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 FT DOMAIN 2643 2656 CARBOHYD.
 FT TRANSMEM 2657 2670 CARBOHYD.
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 FT TRANSMEM 2769 2782 CARBOHYD.
 FT DOMAIN 2783 2796 CARBOHYD.
 FT TRANSMEM 2797 2810 CARBOHYD.
 FT DOMAIN 2811 2824 CARBOHYD.
 FT TRANSMEM 2825 2838 CARBOHYD.
 FT DOMAIN 2839 2852 CARBOHYD.
 FT TRANSMEM 2853 2866 CARBOHYD.
 FT DOMAIN 2867 2880 CARBOHYD.
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 FT DOMAIN 2895 2908 CARBOHYD.
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 FT DOMAIN 2951 2964 CARBOHYD.
 FT TRANSMEM 2965 2978 CARBOHYD.
 FT DOMAIN 2979 2992 CARBOHYD.
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 FT DOMAIN 3007 3020 CARBOHYD.
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 FT DOMAIN 3063 3076 CARBOHYD.
 FT TRANSMEM 3077 3090 CARBOHYD.
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 FT TRANSMEM 3105 3118 CARBOHYD.
 FT DOMAIN 3119 3132 CARBOHYD.
 FT TRANSMEM 3133 3146 CARBOHYD.
 FT DOMAIN 3147 3160 CARBOHYD.
 FT TRANSMEM 3161 3174 CARBOHYD.
 FT DOMAIN 3175 3188 CARBOHYD.
 FT TRANSMEM 3189 3202 CARBOHYD.
 FT DOMAIN 3203 3216 CARBOHYD.
 FT TRANSMEM 3217 3230 CARBOHYD.
 FT DOMAIN 3231 3244 CARBOHYD.
 FT TRANSMEM 3245 3258 CARBOHYD.
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RX MEDLINE-97269065; PubMed-9111065;
 RA Barnes K.V., Cheng G., Dawson M.M., Menick D.R.;
 RT "Cloning of cardiac, kidney, and brain promoters of the feline nrx1
 gene.";
 RL J. Biol. Chem. 272:11510-11517(1997).
 CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
 COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
 SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
 CC -1- ENZYME REGULATION: BY ATP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMMMA.
 CC -----
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 DR EMBL: L35846; AAB41941.1; -
 DR EMBL: U67075; AAB40148.1; -
 DR InterPro: IPR003644; Calx_beta.
 DR InterPro: IPR004836; NaCa_Ext.
 DR Pfam: PF01699; Na_Ca_Ext; 2.
 DR Pfam: PF03160; Calx_beta; 2.
 DR PRINTS: PR01259; NACAEXCHNGR.
 DR SMART: SM00237; Calx_beta; 2.
 DR TIGR: TIGR00845; caca; 1.
 KW transport: Sodium transport;
 KW transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
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RESULT 4
ID NACL_HUMAN STANDARD: PRT: 973 AA
AC P32418: O9UBL8; O9UKX6; O95849; O9UDN1; O9UDN2:
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
GN 1).
OS SLC8A1 OR NCX1 OR CNC.
OC Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Heart;
RX MEDLINE=92262521; PubMed=1374913;
RA Komuro I., Wenninger K.E., Philippson K.D., Izumo S.;
RT "Molecular cloning and characterization of the human cardiac Na+/Ca2+
RT exchanger cDNA";
RT Proc. Natl. Acad. Sci. U.S.A. 89:4769-4773(1992).
RL [2]
RN SEQUENCE FROM N.A. (ISOFORMS 3 AND 7).
RX MEDLINE=21136211; PubMed=11241183;
RA Van Eylen F., Bollen A., Herchevalz A.;
RT "NCX1 Na/Ca exchanger splice variants in pancreatic islet cells";
RL J. Endocrinol. 168:517-526(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 7).
RA Mangini N.J., Chen W., Wang Q., Kennedy B.G.;
RT "Na+/Ca2+ exchanger isoforms in cultured human retinal pigment
RT epithelium";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-603 FROM N.A.
RA Rohlfing T., Stromatt C., Scronce D., Moody T.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 850-973 FROM N.A.
RA Kozlovic A., Stoneking T., Hawkins M., Le T.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 459-681 FROM N.A. (ISOFORM 10).
RA Lundquist P., Lundgren T., Griffl-Linde A., Linde A.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RT "- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
RT SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC "- COUPLING: CA(2+) IS EXCLUDED FROM THE CELL DURING RELAXATION
CC "- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC "- ENZYME REGULATION: BY ATP.
CC "- ALTERNATIVE PRODUCTS: AT LEAST 4 ISOFORMS: 1/NCX1/NCX1.1 (SHOWN
CC HERE), 3/NCX3/NCX1.3, 7/NCX7/NCX1.7 AND 10/NCX10/NCX1.10; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC "- TISSUE SPECIFICITY: CARDIAC SARCOLEMA.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; M91368; AAA35702.1; -
DR EMBL; AF108388; AAF08987.1; -
DR EMBL; AF108389; AAF08988.1; -
DR EMBL; AF128524; AAD26362.1; -
DR EMBL; AC007281; AAF19237.1; -
DR EMBL; AC007254; AAF19235.1; -
DR EMBL; AF155505; AAD17213.1; -
DR PIR; S32815; S32815.
DR Genew; HGNC:11068; SLC8A1.

DR MIM: 182305; Calx_beta.
DR InterPro: IPR004644; NaCa_beta.
DR InterPro: IPR004837; NaCa_beta.
DR InterPro: IPR004836; NaCa_beta.
DR Pfam: PF01699; NaCa_beta; 2.
DR Pfam: PF03160; Calx_beta; 2.
DR PRINTS: P01259; NACAECHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRfam: TIGR00845; caca; 1.
DR Transport; Antiport; Calcium
KW Transmembrane; Glycoprotein; Repeat; Alternative splicing.
KW Calmodulin-binding; Repeat; Alternative splicing.
FT SIGNAL 1 35
FT CHAIN 36 973
FT DOMAIN 36 74
FT TRANSSEM 75 136
FT DOMAIN 97 136
FT TRANSSEM 137 158
FT DOMAIN 159 170
FT TRANSSEM 171 191
FT DOMAIN 192 202
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FT TRANSSEM 229 252
FT DOMAIN 253 272
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FT TRANSSEM 945 961
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FT TRANSSEM 254 273
FT REPEAT 141 181
FT REPEAT 410 481
FT REPEAT 542 612
FT REPEAT 842 878
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FT DOMAIN 692 695
FT DOMAIN 759 763
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FT CARBOHYD 44 44
FT CARBOHYD 160 160
FT CARBOHYD 869 869
FT VARSPLIC 605 613
FT VARSPLIC 619 645
FT VARSPLIC 652 656
FT VARSPLIC 652 679
FT SEQUENCE 973 AA; 108546 MW; 17DFC1B1F15921D8 CRC64;
SO QUERY MATCH
Query Match 71.7%; Score 3439.5; DB 1; Length 973;
Best Local Similarity 68.9%; Pred. No. 1.8e-218;
Matches 674; Conservative 111; Mismatches 128; Indels 65; Gaps 10;
OY 1 MAMLRLOPLTASFLHFGVTVLR--LNGLRABAGSGSDVSTGONNESCAGSSDCKEGV 58
DB 4 MRRSLSPFTSMGPHLLVTVSLSPSHVDHYATETMEEGNETGE---CTGSYYCKKGV 59
OY ILPLIYVPEPSLGDGIKARIVYFVALIYMFGLSIADRFMAISLEVTISOREVTIKPN 118
DB 60 ILPLIYVPEPSLGDGIKARIVYFVALIYMFGLSIADRFMAISLEVTISOREVTIKPN 119
OY 119 GETSTTIRVNETVSNLTALAGSSAPPELLSLIEVCGHGFAGDLGPTIVGSAFNM 178
DB 120 GETTKTIVRIINNETVSNLTALAGSSAPPELLSLIEVCGHGFAGDLGPTIVGSAFNM 179

Qy	179	FIILICICVYVDPDGETRIKIKLRPFETLTAAMSIFAVYIMLVKILAVFSPGVQVWEGILTL	238
Db	180	FIILMLCYVYVDPDGETRIKIKLRPFETLTAAMSIFAVYIMLVKILAVFSPGVQVWEGILTL	239
Qy	239	FEFVPCVLLANVADKRLLFYKVMHKRYKRTDKHRIIETEGEDHPRG--TEMQKMNNSH	239S
Qy	236	---FLDGNLVLPLEGEVD---ESRRKRIIRLKLKKHPRKDDOLVEMANTYALSHQQ	348
Db	300	VENFIDGLV--LEVDERQDDDEARREARLRLLKELKKHPRKLEIOLIELANTYVLSQQQ	358
Qy	349	KSRAFYRQATRMMTGAGNLIKKAAEQAKKASMSSEVHTDEPE-DEISKVFDPDPSYOC	407
Db	359	KSRAFYRQATRMMTGAGNLIKKAADQAKRAVSMHEVNTPEYENDVYSKIFPEQGYIOC	418
Qy	408	LENGCVAILLVVRKRGDKMSKTMVVDYKTEGDSANAGADYEFTGCTVYLKRGEOKEPSVG	467
Db	419	LENGCTVALTLIIRRGGLDTNVFDFPREDTGNAGSDYEFTGCTVYFKRGDQKRIYVG	478
Qy	468	IIDDIFEDDEHFFVRISNVRIIEEQPEGRPAIFNLSPLPRVAVLSPCAVYITLDD	527
Db	479	IIDDIFEDDEHFFVHLSNVASSEASDGLLENHVS--TLACLSPTAVYITFDD	535
Qy	528	HAGITFEPCDPIHVSSEIGVMEVVLRTSGARGVIVPFTVEGTAGGGEDEFTGYEL	587
Db	536	HAGITFEPEPVTNHVSESIGIMEVAVLRTSGARGVIVPYKTIBETARGGGEDEFTDQEL	595
Qy	568	EFKNDEYTKTRKVIYDEEYERODBNFFIALGEPKMMERG-----627	
Db	596	EFONDEIVKTIISVKVIDDEEYKMKTFELEGEPRLVEMSEKKALLNLELGFITGKYL	655
Qy	628	-----ISDVNDRK--LMEEEBAKRIAEEMKPVLGEPHPRKEVI	663
Db	656	FGQPFYKRVYAHREHPIILSTVITTIADIEDDKOPLSKEEBERRIAEKMRPIUGEHTKLEVI	715
Qy	664	IEESEYEFKTVDKLIKKTNLNLVVGTHSMRQDQFMEATVSAAGDEDESGEERLPSCFD	723
Db	716	IEESEYEFKSTVDKLIKKTNLNLVVGTHSMRQDQFMEATVSAAGDEDESGEERLPSCFD	775
Qy	724	YVMHPLTYFMKVLPRACVPTPEYTCGACAFANSLIIGMLTAITIDLASHEGCTIGLKDSV	783
Db	776	YVMHPLTYFMKVLPRAPPTPEYTMNGMACFTYSIMIMLTLAFTIDLASHEGCTIGLKDSV	835
Qy	784	TAVYVARGTSVPPDTPFASKAALDDVYADASIGNVTSNANVPELIGILAMSVAAIYMAL	843
Db	836	TAVYVARGTSVPPDTPFASKAATDDQIADASIGNVTSNANVPELIGILAMSVAAIYHAA	895
Qy	844	QGOEHEVSAGTLAESVTLFTITFAFVCIISVLLYRRRPHLIGELGPRGCKLATTWVLEFSLM	903
Db	896	NCEGQKVSPTGLARSVTLFTITFAFVCIISVLLYRRRPHLIGELGPRRAKLLTSCLPFLWM	955
Qy	904	LLYIFATLEAYCIYIKGF 921	
Db	956	LLYIFSSLEAYCHIKGF 973	
RESULT 5			
NACL_CAVPO			
ID	NACL_CAVPO	STANDARD:	PRT: 970 AA.
AC	P48766;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, last annotation update)		
DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).		
GN	SIC8A1.		
OS	Cavia porcellus (Guinea pig).		
OC	Eukaryota: Metazoa: Chordata: Craniala: Vertebrata: Euteleostomi:		
OC	Mammalia: Eutheria: Rodentia: Hystricognathi: Caviidae: Cavia.		
ON	NCBI_TaxID=10141;		
FN	[1]		

Query Match 71.6%; Score 3432.5; DB 1; Length 970;
 Best Local Similarity 68.7%; Pred. No. 5.1e-218;
 Matches 672; Conservative 112; Mismatches 129; Indels 65; Gaps 11;

```

QY 1 MAMLRQPLTSLAFH-FGLVTVL-FLNGLRAAGSGDVPSTGQNNESCGSSDCKEYV 58
DB 1 MRLSLSPYSLGFLHLLAMTLLSHVDHITAE---EMVEGNETGCTGCTGYCKKV 56
QY 59 ILPIVPEPSPSGDKARIYVFAVLIYFVGLVSTIADPFMASTIEYTSQERVTIKKN 118
DB 57 ILPIVPEPSPSGDKARIYVFAVLIYFVGLVSTIADPFMASTIEYTSQERVTIKKN 116
QY 119 GETSTTTIYNNETVSNLTMALGSSAPILLSLIEVCHGFAGDLGSTIYGAFAFN 178
DB 117 GETTTTIVNNETVSNLTMALGSSAPILLSLIEVCHGFAGDLGSTIYGAFAFN 176
QY 179 FTITIGCVVVDGETRIRIKHLRPEITAMSTIFAYIMLILAVFSPGVOMEGILT 238
DB 177 FTIILACVYVVDGETRIRIKHLRPEITAMSTIFAYIMLILAVFSPGVOMEGILT 236
QY 239 FEPPVCVLLANVADRLLFYKYMHHKYYRDKHRTGIIIEGHPKC---IENDGKMNH 295
DB 237 FEPPVCVLLANVADRLLFYKYMHHKYYRDKHRTGIIIEGHPKC---IENDGKMNH 296
QY 296 ---FLDGNLVPEKGEVD---ESRREMITLKDOKHPEKDLDOLEVANYALSHOO 348
DB 297 VNFPLDGNLV-LEVEDERODDEEARREMARILKELKOKPEKEIDELILANTYLSOO 355
QY 349 KRAFYRIQATMTMGAGNILKHAQAQKASMSSEVHTDEP-DEFISKEFDPSCSYOC 407
DB 356 KRAFYRIQATMTMGAGNILKHAQAQKASMSSEVHTDEP-DEFISKEFDPSCSYOC 415
QY 408 LENCAGVILTVVRKGGDMKMTYVDKTEDSGANAGADVEFEGTYVLRPGEFQKFSVG 467
DB 416 LENCAGVILTVVRKGGDMKMTYVDKTEDSGANAGADVEFEGTYVLRPGEFQKFSVG 475
QY 468 IIDDDIFEDDEHFVRLSNVRIEEOPEEGMPALFNSLPLRAVLASCVATVITLDD 527
DB 476 IIDDDIFEDDEHFVRLSNVRIEEOPEEGMPALFNSLPLRAVLASCVATVITLDD 532
QY 528 HAGITFEEDDTLHVSESTIVMEKVLRTSGANGTVIVPRVEGAKGGEDFEDTYGEL 587
DB 533 HAGITFEEDDTLHVSESTIVMEKVLRTSGANGTVIVPRVEGAKGGEDFEDTYGEL 592
QY 588 EKNNETVTVIRKIVDESEYERQENFIALGEPKMMENG----- 627
DB 593 EKNNETVTVIRKIVDESEYERQENFIALGEPKMMENG----- 652
QY 628 -----ISDVTDRK--LTMEEPKAKRIAEWGKPVLGHPKLEYI 663
DB 653 YGQPVLRKYNHARDHPIPTVITIADEYDOKPLTSKEEERKRIAEGRILGEBTKLEYI 712
QY 664 IESEYEFKTTVDKLKIKTNALVGVTHSWRDQFMEATYVSAAGDEDEDESGEBRLPSCD 723
DB 713 IESEYEFKTTVDKLKIKTNALVGVTHSWRDQFMEATYVSAAGDEDEDESGEBRLPSCD 772
QY 724 YMHHLTVWKKLACVPRTEYCHGACPAVSILLIGMTATITIGLASFPCTIGLKDSY 783
DB 773 YMHHLTVWKKLACVPRTEYCHGACPAVSILLIGMTATITIGLASFPCTIGLKDSY 832
QY 784 TAVVEVAFGSTVDFTFASKAALODVYADASIGNVTSNANVVFGLIGLAMSVAATYVNL 843
DB 833 TAVVEVAFGSTVDFTFASKAALODVYADASIGNVTSNANVVFGLIGLAMSVAATYVNL 892
QY 844 OGOEYHVSAGTLAFSVTLFTTAFCISVLYLRPHLGGELGPGCKLATVTLFVSLM 903
DB 893 NEOEKVSPGTLAFSVTLFTTAFCISVLYLRPHLGGELGPGCKLATVTLFVSLM 952
QY 904 LLYILFATLEAYCYIKGF 921
DB 953 LLYILFATLEAYCYIKGF 970

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RESULT 6
ID NA1_NAC1_RAT STANDARD: PRT: 971 AA.
AC 001728;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DE 1).
GN SLC8A1 OR NCX1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=93138118; PubMed=8422940;
RA Low W., Kasir J., Rahamimoff H.;
RT "Cloning of the rat heart Na(+)-Ca2+ exchanger and its functional
RT expression in HeLa cells.";
RL FEBS Lett. 316:63-67(1993).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=93202244; PubMed=8454039;
RA Furman I., Cook O., Kasir J., Rahamimoff H.;
RT "Cloning of two isoforms of the rat brain Na(+)-Ca2+ exchanger gene
RT and their functional expression in HeLa cells.";
RL FEBS Lett. 319:105-109(1993).
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney cortex;
RX MEDLINE=94253030; PubMed=8195112;
RA Lee S.-L., Yu A.S.-L., Lytton J.;
RT "Tissue-specific expression of Na(+)-Ca2+ exchanger isoforms.";
RL J. Biol. Chem. 269:14849-14852(1994).
RN [4]
RP TISSUE SPECIFICITY.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=96394663; PubMed=8798769;
RA Nicoli D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA Philipson K.D.;
RT "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
RL J. Biol. Chem. 271:24914-24921(1996).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
CC COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION
CC SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -1- ALTERNATIVE PRODUCTS: 5 isoforms; heart/NCX1 (shown here),
CC brain 1/NCX5, brain 2/NCX4, kidney 1/NCX7 and kidney 2/NCX3;
CC are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMA OR BRAIN, AND SPLEEN.
CC -----
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CC entities requires a license agreement (see http://www.isb-sdb.ch/announce/
CC or send an email to: license@sdb-sdb.ch).
CC -----
DR EMBL: X68191; CAA48273.1; -
DR EMBL: X68812; CAA48707.1; -
DR EMBL: X68813; CAA48708.1; -
DR EMBL: U04933; AAB39952.1; -
DR EMBL: U04934; AAB19124.1; -
DR EMBL: U04936; AAA19125.1; -
DR PIR: S25552; S25552.
DR PIR: S28833; S28833.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NacCa_Extmemb.

```

DR	InterPro:IPR004836; Na,Ca_Ex.			
DR	Pfam: PF01699; Na,Ca_Ex; 2.			
DR	Pfam: PF03160; Calx-beta; 2.			
DR	PRINTS; PRO1259; NACACXCHNGR.			
DR	SMART; SM00237; Calx_beta; 2.			
DR	TIGRFAMs; TIGR00845; Caca; 1.			
KW	Transport; Anliport; Calcium			transport; Sodium transport;
KW	Transmembrane; Glycoprotein; Signal;			
KM	Calmodulin-binding; Repeat; Alternative splicing.			
FT	SIGNAL	1	32	POTENTIAL.
FT	CHAIN	33	971	SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN	33	71	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	72	93	POTENTIAL.
FT	DOMAIN	94	133	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	134	155	POTENTIAL.
FT	DOMAIN	156	167	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	168	188	POTENTIAL.
FT	DOMAIN	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	DOMAIN	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	DOMAIN	250	770	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	771	790	POTENTIAL.
FT	DOMAIN	791	797	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	798	820	POTENTIAL.
FT	DOMAIN	821	822	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	823	841	POTENTIAL.
FT	DOMAIN	842	872	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	873	893	POTENTIAL.
FT	DOMAIN	894	904	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	905	925	POTENTIAL.
FT	DOMAIN	926	942	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	943	959	POTENTIAL.
FT	DOMAIN	960	971	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	971	270	ALPHA-1.
FT	DOMAIN	251	178	BETA-1.
FT	REPEAT	138	478	BETA-2.
FT	REPEAT	407	478	ALPHA-2.
FT	REPEAT	539	609	POLY-PHE.
FT	REPEAT	840	876	POLY-GLU.
FT	DOMAIN	236	239	POLY-ASP.
FT	DOMAIN	690	693	PHOSPHORYLATION (BY SIMILARITY).
FT	DOMAIN	757	761	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	MOD_RES	389	389	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	867	867	TSISYVIDEEXEKKNFTFIFGEIRLVENSEKK -> ITT
FT	VARSPLIC	602	635	IRFDEEYERKSCSFLVEPKMTIRGKK (IN KIDNEY
FT				ISOFORM 1 AND KIDNEY ISOFORM 2).
FT	VARSPLIC	636	642	MISSING (IN BRAIN ISOFORM 1, BRAIN
FT				ISOFORM 2, KIDNEY ISOFORM 1 AND KIDNEY
FT	VARSPLIC	649	654	MISSING (IN BRAIN ISOFORM 1 AND KIDNEY
FT	VARSPLIC	649	677	MISSING (IN BRAIN ISOFORM 2 AND KIDNEY
FT	CONFLICT	250	250	D -> A (IN REF. 1).
FT	CONFLICT	402	402	P -> A (IN REF. 1).
SO	SEQUENCE	971 AA; 108184 MW;		EC456CFE3AFC6A9 CRC64;

Query Match	71.58;	Score 3428;	DB 1;	Length 971;
Best Local Similarity	68.78;	Pred. No. 1e-217;		
Matches 675;	Conservative 106;	Mismatches 124;	Indels 78;	Gaps 11

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Oy 4 LRLQGLTSAFHFHGFQVFLVLT-----NGLFAEAGSGSDVSTGONNESCAGSSDK 55
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 2 LRLSLPVPVSMGFRVYTLVALLFTHVHDITADTAEALGNG-----ENTTECGSYCK 53
Oy 56 EGVLLPIRYPPNPSPSGDKIAIIVYYPALLIMELGVSIINDRFMASTEIVTTSQREYTIK 115
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 54 KGVILPIHEPDPSPSGDKIAIATVYFAAMVMEGVSIINDRFMSSTEIVTTSQREKTIK 113
Oy 116 KPNCESTSTTITRVNVEVYSNLTJMALCGSSAPELLLSIEVCGHGFIAGDGLPSTIVGSA 175

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Dd	114	KPNGETTQTYIRKINNEYNSLTLMALOSSAPEILLSVIEVGNHFTAGDGLGPSTVGSAA	173
Qy	176	FNMFTIGICVYVJPDGETRKIKHLRYEFTTAANSIFAUYIMILAVSPGVQWEGCL	235
Dd	174	FNMFTIILACVYVDPDGETRKIKHLRYEFTVAAMSIFAUYIMYLITLSSVPGVAVEWGL	233
Qy	226	LTLFEPACVILVAADOKRLLFYUYMKKTYTODHNRGIIITBEDDHPKG---TEMOSKM	292
Dd	234	LLEFFFLVCYFAMWADRLLTFTYKTRIRAGOKRMIIENHESDRAPSTETEMDSKV	293
Qy	293	NSH---FLDGNLVLPLEGKVD---ESHREMIIRILKDLKOKHPEKDLDOLEVANYYALS	345
Dd	294	NSHVDNFIJDGALV---LEVDERQDDDEBARREMARILTELKOKHPEKEIOELIETLANQVLS	352
Qy	346	HOQKSAFAYRIQATRMATGAGNILLKHAADOKAKASSKSEYHNDDEP-DPISKVFEDPCS	404
Dd	353	QOQKSAFAYRIQATFRLMAGNIIILKHAADOKARAKVAMHEHNMVDVENDSVSKFEEOGT	412
Qy	405	YQCLENGCAVLLTVYRKGDGSKMUYDYKREDCSANAAGADYETBETVYLKGEPOKEF	464
Dd	413	YQCLENGCTVALTLIIRRGDILNTNPFVDEREDSTANAGSYETBETVILFKPEOTKEI	472
Qy	465	SVGIIDDDIIFEDEHEFFRLNSVRIIEEOPEREGPPAIFNSLPLR-AVLASPCVATVTI	523
Dd	473	RNGIIDDIDIFEDEHEFFLHLSNVAVSSVSDG---ILDSNHSAIACLGSPMTATITI	528
Qy	524	LDDHAGJTFTECDTIHVSISIGMEVKVLTSGARGTVJPFPTVHGIAKGGGEDEDT	563
Dd	529	FDDDHAGJTFTEEPRTYHVSISIGIMEYVLTSGARKNVJIPYKTIETGTARGGGEDEDT	568
Qy	564	YGELEFKNDEMYKTRIVYVDEEYERQENEFILGEPKMKR-----	626
Dd	569	CGELEFQNDDELKTVISVYVDEEYERKMTFFIEIGERPLWSEKKALLNLNEGTTLT	648
Qy	627	-----GISDVTDKR---LTMEEBEAKRIAEMKGPVLOENP	658
Dd	649	BEGKMYGQPVPRKYNHARHPIRPSYVISISEYDDKOPLTSEEBERLIAEMGRPIIENHT	708
Qy	659	KLEVTIIESYERKTTVDKLIKLTNALVYGTHSRRDOPMEATITVYSAAGDEDEDESGERL	718
Dd	709	KLEVTIIESYERKSTVDKLIKLTNALVYGTHSRRDOPMEATITVYSAEEDDDDECCEKEL	768
Qy	719	PSCFPYVNHFLTFVKVLYFACVUPREYCHGACPAVSLIIGMTLITIGLASHFGCTIG	778
Dd	769	PSCFPYVNHFLTFVKVLYFACVUPREYCHGACPAVSLIIGMTLITIGLASHFGCTIG	828
Qy	779	LKDSYAVVFAVFGSVYDTPFASKAALODVYVADASIGNVTGSNAVVFILGIGLAVSAA	838
Dd	829	LKDSYAVVFAVFGSVYDTPFASKAALODVYVADASIGNVTGSNAVVFILGIGLAVSAA	888
Qy	839	IYVALOGOEHFVHSACTLAFSVTLTPIFAVYISVLLYRRRHLOGELGGRGCKLATIWL	898
Dd	889	IYHANGEDQFKVSPQTLAFSVTLTPIFAVYINVGVLRYRRREIPEGELGGRGCKLATIWL	948
Qy	899	FVSLMLYLTIFATLEAYKIGCF 921	
Dd	949	FVLLMLYLTIFESSLEAYCHIGCF 971	

	RESULT 7		
NACL_BOVIN			
ID	NACL_BOVIN	STANDARD;	PRT; 970 AA.
AC	P48765;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).		
GN	SLC8A1.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		

OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=93037494; PubMed=1416984;
RA Aceto J.F., Condrescu M., Kroupis C., Nelson H., Nelson N.,
RN Nicoll D.A., Phillips K.D., Reeves J.P.;
RT "Cloning and expression of the bovine cardiac sodium-calcium
exchanger.";
RL Arch. Biochem. Biophys. 298:553-560(1992).
RN [2]
RP SUBCELLULAR LOCATION.
RC TISSUE=Retinal rod cell;
RX MEDLINE=90241959; PubMed=2334719;
RA Reid D.M., Friedel U., Moiday R.S., Cook N.J.;
RT "Identification of the sodium-calcium exchanger as the major
ricin-binding glycoprotein of bovine rod outer segments and its
localization to the plasma membrane.";
RL Biochemistry 29:1601-1607(1990).
CC -1- COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING CONTRACTION
SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.
CC -1- ENZYME REGULATION: BY ATP.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
CC -1- TISSUE SPECIFICITY: CARDIAC SARCOLEMMMA.
CC -----
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CC -----
DR EMBL; L06438; AAA30509.1; -
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; Na_Ca_Ex.
DR Pfam: PF03160; NaCa_Ex; 2.
DR Pfam: PF03160; Calx_beta; 2.
DR PRINTS: PRO1259; NACAEXCHNGR.
DR SMART: SM00237; Calx_beta; 2.
DR TIGRFAMs: TIGR00845; caca; 1.
KW Transport: Antiport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL 1 32
FT CHAIN 33 970
FT DOMAIN 33 71
FT TRANSSEM 72 93
FT DOMAIN 94 133
FT TRANSSEM 134 135
FT DOMAIN 156 167
FT TRANSSEM 168 188
FT DOMAIN 189 199
FT TRANSSEM 200 222
FT DOMAIN 223 225
FT TRANSSEM 226 249
FT TRANSSEM 250 269
FT DOMAIN 270 789
FT TRANSSEM 790 796
FT TRANSSEM 797 819
FT DOMAIN 820 821
FT TRANSSEM 822 840
FT DOMAIN 841 871
FT TRANSSEM 872 892
FT DOMAIN 893 903
FT TRANSSEM 904 924
FT DOMAIN 925 941
FT TRANSSEM 942 958
FT DOMAIN 959 970
FT DOMAIN 251 270

FT REPEAT 138 178 ALPHA-1.
FT REPEAT 407 478 BETA-1.
FT REPEAT 539 609 BETA-2.
FT REPEAT 839 875 ALPHA-2.
FT DOMAIN 236 292 POLY-PHE.
FT DOMAIN 689 692 POLY-GLU.
FT DOMAIN 756 760 POLY-ASP.
FT MOD_RES 389 389 PHOSPHORYLATION (POTENTIAL).
FT CARBOHYD 41 41 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 866 866 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 970 AA; 108027 MW; 7C29153D1F87DDBE CRC64;

Query Match 71.4%; Score 3425.5; DB 1; Length 970;
Best Local Similarity 68.7%; Pred. No. 1,35e-217;
Matches 672; Conservative 110; Mismatches 131; Indels 65; Gaps 10;

1 MAMLRQPLTSAFLHFGVTFVLV--LNGLRKAGSGSDVPSGQNNMSSGSSDCKEGV 58
1 MQLFSLSTPLSGFHVIAAMVALLFESHVDHISKFTMBEGNETGE----CTGSIYCKRGV 56
59 ILPIWYENPNSLGDKRIARVIVYFVALIYFGLGVSIIADRFMAISIVTSQEREVTIKRPN 118
57 ILPIWEPQDPSFGDKIARATYFVAMVYFGLGVSIIADRFMSISIVTSQEREVTIKRPN 116
119 GETSTTIRVNNVETVSNLTIALMGSSAPEILLSLVCGHGIGIADLDGPSTIVGSAAFNM 178
117 GETTIVIRVNNVETVSNLTIALMGSSAPEILLSLVCGHGIGIADLDGPSTIVGSAAFNM 176
179 FLIIGICVYVDPGSTRKIKHLRVFFITAAWSIFAYIMLYMILAVFSPGVQVWEGILTL 238
177 FLIILACVYVDPGSTRKIKHLRVFFITAAWSIFAYIMLYMILAVFSPGVQVWEGILTL 236
239 FFFPVCVLLAVADKRLLFYKMKKRYTDKRGIIETEGDHPKG---IEMDGKMMNSH 295
237 FFFPVCVVFAWADKRLLFYKMKKRYTDKRGIIETEGDHPKG---IEMDGKMMNSH 296
236 ---FLDGNLVPLEGKVD---ESRREMIIRIKDKOKNHPREDLDOLVEMAYVYALSHQ 348
297 VDSFLDGAIV-LEDERQDDEEARERMAIRIKELKOKNHPREDLDOLVEMAYVYALSHQ 355
349 KSRAFYRIQATRMGTAGNIILKHAEOAKKASSSEVHTDEPE-DFTSKYFFDPCSYQC 407
356 KSRAFYRIQATRMGTAGNIILKHAEOAKKASSSEVHTDEPE-DFTSKYFFDPCSYQC 415
408 LENCAGVLLVYVRKGGDSKTYVDYKTEDGSANAGADYEFTGTVVLKPGTQREFSVG 467
416 LENCSTVALLTIIRGGDLTNVFDPRTEEDGANAGSDYEFTGTVVFKPGTQREIRVG 475
468 IIDDIFEDDEHFVRLSNVRIEEOQREEMPRALFNSLPLPRAVLASPCVATVITLDD 527
476 IIDDIFEDDEHFVRLSNVRIEEOQREEMPRALFNSLPLPRAVLASPCVATVITLDD 532
528 HAGITFEPCDRIHVSISIGVMEVKYLRTSGAGTVIVFPRVEGTAKGGDEFDYTEL 587
533 HAGITFEPCDRIHVSISIGVMEVKYLRTSGAGTVIVFPRVEGTAKGGDEFDYTEL 592
588 EKKNDVTKTRVKTIVDEEYERQENFTALGEPKMERG----- 627
593 EFNQNDVTKTRVKTIVDEEYERQENFTALGEPKMERG----- 652
628 -----ISDVTDRK--LTMESEAKRIAMGKPVJGEMHKLVI 663
653 YGQVFRVVAHREHPLSTITITADEYDKQPLTSKEEERIAMGRPIIGEHRLREVI 712
664 IEESEFTYTDKLIKTKTNLALVGTSHMRDQFMATVYSAAGDEDESGEERLPSCFD 723
713 IEESEFTYTDKLIKTKTNLALVGTSHMRDQFMATVYSAAGDEDESGEERLPSCFD 772
724 YVMEFLVFWKVLFAFVCPTEYCHGMAFVSIILIGMLTALIGDLASHFGCTIGLKDSV 783
773 YVMEFLVFWKVLFAFVCPTEYCHGMAFVSIILIGMLTALIGDLASHFGCTIGLKDSV 832

Oy	784	TAYVAVAGTSTVPDFFASKAALADGVADASIGNTGSAVNATVFGLIAMSVALITYMAL	843
Dd	833	TAYVAVAGTSTVPDFAFSKVAATIDQOYDASIGNTGSANAVNVLGIIVANSIAITRYAA	892
Oy	844	QGQEFHVASGTLAESVTLTFTTFAPVCISVLLYRRRPHLGGELIGPRGCKLATWTLVSVLM	903
Dd	893	NCEQKVPSPGTLAEFSVTLTFTTFEAFNVGVLLYRRRPRIEGELIGPRTAKLITLSCLFVLM	952
Oy	904	LXLYLFATLFAVCYTKGF	921
Dd	953	LXLYFSSLEACHTKGF	970
RESULT 8			
ID	NACL_MOUSE	STANDARD:	PRT: 970 AA.
AC	p70414.		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).		
	SIC8A1 OR NCX.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Cranialta; Vertebrate; Euteleostomi;		
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A..		
RC	STRAIN=C57BL/6;		
RX	MEDLINE=96250070; PubMed=8659820;		
RA	Kim I., Lee C.O.;		
RT	"Cloning of the mouse cardiac Na(+)-Ca2+ exchanger and functional expression in xenopus oocytes."		
RL	Ann. N.Y. Acad. Sci. 779:126-128(1996).		
CC	-1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS TO PREVENT OVERLOADING OF INTRACELLULAR STORES.		
CC	-1- ENZYME REGULATION: BY ATP.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.		
CC	-1- TISSUE SPECIFICITY: CARDIAC SARCOLEMMA.		
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CC	EMBL: U70033; AAB46708.1; -.		
DR	MCD; MGI:107956; SIC8A1.		
DR	InterPro: IPR003644; Calx_beta.		
DR	InterPro: IPR004837; NaCa_Exmemb.		
DR	InterPro: IPR004836; Na_Ca_Ex.		
DR	Pfam: PF01699; Na_Ca_Ex; 2.		
DR	Pfam: PF03160; Calx-beta; 2.		
DR	PRINTS: PR01359; NACAEXCHNR.		
DR	SMART: SM00237; Calx_beta; 2.		
DR	TIGRFAMs: TIGR00845; caca; 1.		
KW	transport; Antiport; Calcium		
KW	Transmembrane; Glycoprotein;		
KW	Calmodulin-binding; Repeat.		
FT	SIGNAL	1	32
FT	CHAIN	33	970
FT	DOMAIN	33	71
FT	TRANSSEM	72	93
FT	DOMAIN	94	133
FT	TRANSSEM	134	155
FT	DOMAIN	156	167
FT	TRANSSEM	168	188
FT	DOMAIN	189	199
FT	TRANSSEM	200	222
FT	POTENTIAL.		
FT	SODIUM/CALCIUM EXCHANGER 1.		
FT	EXTRACELLULAR (POTENTIAL).		
FT	POTENTIAL.		
FT	CYTOSOLSMIC (POTENTIAL).		
FT	POTENTIAL.		
FT	EXTRACELLULAR (POTENTIAL).		
FT	POTENTIAL.		
FT	CYTOSOLASMIC (POTENTIAL).		
FT	POTENTIAL.		

FT	DOMAIN	223	225		EXTRACELLULAR (POTENTIAL) .
FT	TRANSSEM	226	249		POTENTIAL.
FT	DOMAIN	250	769		CYTOPLASMIC (POTENTIAL) .
FT	TRANSSEM	770	789		POTENTIAL.
FT	DOMAIN	790	796		EXTRACELLULAR (POTENTIAL) .
FT	TRANSSEM	797	797		POTENTIAL.
FT	DOMAIN	820	821		CYTOPLASMIC (POTENTIAL) .
FT	TRANSSEM	822	840		POTENTIAL.
FT	DOMAIN	841	871		EXTRACELLULAR (POTENTIAL) .
FT	TRANSSEM	872	892		POTENTIAL.
FT	DOMAIN	893	903		CYTOPLASMIC (POTENTIAL) .
FT	TRANSSEM	904	924		POTENTIAL.
FT	DOMAIN	925	941		EXTRACELLULAR (POTENTIAL) .
FT	TRANSSEM	942	958		POTENTIAL.
FT	DOMAIN	959	970		CYTOPLASMIC (POTENTIAL) .
FT	TRANSSEM	251	270		CALMODULIN-BINDING (POTENTIAL) .
FT	REPEAT	138	178		ALPHA-1.
FT	REPEAT	407	478		BETA-1.
FT	REPEAT	539	609		BETA-2.
FT	REPEAT	839	875		ALPHA-2.
FT	DOMAIN	236	239		POLY-PHE.
FT	DOMAIN	689	692		POLY-GLU.
FT	DOMAIN	756	760		POLY-ASP.
FT	MOD_RS	389	389		PHOSPHORYLATION (POTENTIAL) .
FT	CARBOHYD	41	41		N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	157	157		N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	CARBOHYD	866	866		N-LINKED (GLCNAC. . .) (POTENTIAL) .
FT	SEQUENCE	970 AA;	108035 MW;	F5FC0BD072B6602 CRC64;	
Query Match					71.08; Score 3405.5; DB 1; Length 970;
Best Local Similarity					68.38; Pred. No. 3.1e-216;
Matches 665; Conservative 111; Mismatches 138; Indels 59; Gaps					
OY	4	LRLDPLTSAFHFEGLVLFVFLFLNGLRAEAGSGGCVSPSTGONNESGSGSSDCKEGVLLPIW	63		
Db	2	LRLSLPRTVSMGFFLVALLVALLFHVNDHITADFAELNGNTEETGSGYCKKGVLLPIW	61		
OY	64	YRPNDSLGDKTARVIVYVFVALIYFLGVSTIADRFMASIEYITISOEBEYITIKKPNGETST	123		
Db	62	EPDPSFEDCKTARATVYFVAWVYFELVSTIADRFMSIEYITISOEKETIKKPNGETTK	121		
OY	124	TTIRVWNTVSNLTLMLGSSAPRLLSLLEVCGHGTIAGLGGSTVGSAAFMFTIIG	183		
Db	122	TTVRWNTVSNLTLMLGSSAPRLLSLLEVCGHNTAAGDLGRSTVGSAAFMFTIIA	181		
OY	184	ICVYVYPDGETRIKHLRVEPTTAAMSIFAYIMLYMILAVFSPGVOWMEGLLTLEFPV	243		
Db	182	LCVYVYPDGETRIKHLRVEPTTAAMSIFATWLYIILSVSSPGVWVMEGLLTFFFEPI	241		
OY	244	CVLLAVWADRKLTLFYKKWKKKFKPRDKRGIIITIEHSGHPKG--IENDGKMMNSH--FL	297		
Db	242	CVLRWADRKLTLFYKKYKKYKPRGKRGKGMIIIEHGRPRPSKTEIENDGKVVNSHDNFL	301		
OY	298	DGNLVPLEGGFVD---ESRREMRIILDKQKHREKLDOLVEMANYVALSHQOCSR	353		
Db	302	DGALV-LEVDERRDDDEAREARREMARILKELOKHPKEIKQIETILAYVQLSQOQCSR	360		
OY	354	YRIQATIRMTAGNIIKKHADEQKKKSSMBEVIITDDEP-DFTSKVTFPDCSVQCLENG	412		
Db	361	YRIQATIRMTAGNIIKKHAADQRRKVVSMIEVMEKMAENDPVRKIFEEGTVQCLENG	420		
OY	413	AVLLTVNKGKGMKMTKVDYKTKEDGSANAGADVEFTEGTVLVKPGTQKEFSGIIDD	472		
Db	421	TVALTIRMGKGLDSTIYFVNDPTREDGTANAMASDVELEFGVYIKPRGTQKEINVIIDD	480		
OY	473	IFEEDEHEFVRLSNVRIIEEQPEEGMPAIFNSILPRAVLASPCVATVITLDDHAGIF	532		
Db	481	IFEEDEHNLVHLSNVRVSSDSEGI--LESNHAASSIACLGSTATITITIFDDHAGIF	537		
OY	533	TFEEDTTHVSSISGVMEKVLRTSGAGTVVPRPTGAKGSGGEFDTYELERKND	592		
Db	538	TFEEDTVHVSISIGIMEKVLRTISGAGNVAIIPKLTETGARGGGEPDFTGCPPEFOND	597		

[illegible]

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RESULT 9
NAC2_HUMAN
ID NAC2_HUMAN STANDARD: PRI: 921 AA.
AC Q9UPR5:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
2).
GN SLC8A2 OR NCX2 OR RTAA1087.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99397452; PubMed=10470851;
RA Kikuno R., Nagase T., Ishikawa K.-I., Hiroseawa M., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XIV.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 6:197-205(1999).
CC -1- FUNCTION: RAPIDLY TRANSPORTS CA2+ DURING EXCITATION-CONTRACTION
CC COUPLING. CA(2+) IS EXTRUDED FROM THE CELL DURING RELAXATION SO AS
CC TO PREVENT OVERLOADING OF INTRACELLULAR STORES (BY SIMILARITY).
CC -1- ENZYME REGULATION: BY ATP (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -----
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CC -----
DR EMBL: AB029010; BAAB3039.1. ALT_INIT.
DR Genew: HGCNC:11069; SLC8A2.
DR MIM: 601901.
DR InterPro: IPR003644; Calx_beta.
DR InterPro: IPR004837; NaCa_Exmemb.
DR InterPro: IPR004836; NaCa_Ex.
DR

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DR	Pfam: PF01699; Na,Ca,Ex: 2.	
DR	Pfam: PF03160; Calx-beta: 2.	
DR	PRINTS: PRO1259; NACATXCHNGR.	
DR	SMART: SM00237; Calx, beta: 2.	
DR	TIGRFams: TIGR00845; beta: 1.	
KW	Transport; Antipor; Calcium	transport; Sodium transport;
KW	Transmembrane; Glycoprotein;	phosphorylation; signal;
KW	Calmodulin-binding; Repeat.	
FT	SIGNAL	1 20
FT	CHAIN	21 921
FT	DOMAIN	21 68
FT	TRANSSEM	69 90
FT	DOMAIN	91 130
FT	TRANSSEM	131 152
FT	DOMAIN	153 164
FT	TRANSSEM	165 185
FT	DOMAIN	186 196
FT	TRANSSEM	197 219
FT	DOMAIN	220 222
FT	TRANSSEM	223 246
FT	DOMAIN	247 720
FT	TRANSSEM	721 740
FT	DOMAIN	741 747
FT	TRANSSEM	748 770
FT	DOMAIN	771 772
FT	TRANSSEM	773 791
FT	DOMAIN	792 822
FT	TRANSSEM	823 843
FT	DOMAIN	844 854
FT	TRANSSEM	855 875
FT	DOMAIN	876 892
FT	TRANSSEM	893 921
FT	DOMAIN	910 921
FT	DOMAIN	248 267
FT	REPEAT	135 175
FT	REPEAT	397 468
FT	REPEAT	527 597
FT	REPEAT	790 826
FT	DOMAIN	29 32
FT	DOMAIN	638 641
FT	CARBOHYD	34 34
FT	CARBOHYD	817 817
EQ	SEQUENCE	921 AA; 100367 MW; 798CDE7E32B9410C CRC64;

Query Match	70.3%	Score 3373.5	DB 1	Length 921
Best Local Similarity	71.0%	Pred. No. 3.6e-214		
Matches 638	Conservative 124	Mismatches 104	Indels 33	Gaps 9

QY	40	STGQNNESCSCGSDKEGVLPWPENPSSLDKTAIVIVYVALIYMLGVSIADREM	99
		: : : : : : : : : : : : : : : : : : : :	
Db	39	STG-----GCQSYRCQPGVLLPVMRPDDPSLDKAARAVVYVAVMYMLGVSIADREM	94
QY	100	ASIEVITSOEREVYTKTRPGETSTTTIRYMNVTVSNTLMALGSSAPETLLSIEYCGHG	159
		: : : : : : : : : : : : : : : : : : : :	
Db	95	AAIEVITSEKEKITTKANGERTSVGTIRIMETVSNLTLMALGSSAPETLLSIEYCGHN	154
QY	160	FLAGLGSTVIGSAFAMFPIIGCVVYIPRGEPRTKIKHLVFPFTLWMSIFAYTWLM	219
		: : :	
Db	155	FQAGLGSTVIGSAFAMFVYIAVCITYIPAGESRKIKHLVFPFTLWMSIFAYTWLM	214
QY	220	ILAVFSPGVOWEGILLTFPPVCVLLAWADKRYLFKYKMHKKYRTDKNGIILIEETBG	279
		: : :	
Db	215	ILAVFSPGVOWEALLTLVFPVCVLFVAMADKRYLFKYKYYKRTDPRSGIILGABG	274
QY	280	DHPKGIEMDGKMMNHFLDGNL-----VPLEKEVYDESKREIRILKDKQNHPEKDLDO	334
		: : : : : : : : : : : : : : : : : : : : : : :	
Db	275	DHPKSIELDGTFFVGE-APGELGSGPRAERELDASRREYIQLIKDKQNHPEKDLDO	333
QY	335	LYEMANVYALSHOOKSRAFYRTOATRRMTGAANIILKHNABQAKASSSEVHTDERPE	394
		: : :	
Db	334	LVGINVYALLHQKSRAFYRIQATRLMTGAGNVLRHNAAADSRRRAAPREGADE-DBG	392
QY	395	ISKVEFDSCSYQCLENGCAVLLTVVRKGDMSKTMIVDYKTEGDSANAGADYEETEGTVV	454


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CC or send an email to license@slb-slb.ch).
CC -----
DR EMBL: AF062921: AAC16732.1: -
DR EMBL: AF062922: AAC77912.1: -
DR EMBL: AF026132: AAB7832.1: -
DR EMBL: AB014602: BAA31677.1: ALT_SEQ.
DR Genew: HGNC:10975: SLIC24A1.
DR MIM: 603617: -
DR InterPro: IPR004817: K_NaCaexchang.
DR InterPro: IPR004837: NaCa_Exmemb.
DR Pfam: PF01699: Na-Ca-Ex: 3.
DR TIGRFAMs: TIGR00367: K_NaCaexchang-rel: 1.
DR TIGRFAMs: TIGR00927: 2A1904: 1.
DR Vision: Transport: Antipor: Symport: Calcium transport:
KW Transmembrane: Glycoprotein: Phosphorylation: Signal: Repeat:
KW Alternative splicing.
KW SIGNAL
FT CHAIN 1 38
FT DOMAIN 39 1099 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT TRANSMEM 39 452 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 453 473 POTENTIAL.
FT TRANSMEM 474 497 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 498 518 POTENTIAL.
FT TRANSMEM 519 522 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 523 543 POTENTIAL.
FT TRANSMEM 544 563 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 564 584 POTENTIAL.
FT TRANSMEM 585 585 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 586 606 POTENTIAL.
FT TRANSMEM 607 907 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 908 928 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 929 935 POTENTIAL.
FT TRANSMEM 936 956 POTENTIAL.
FT TRANSMEM 957 971 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 972 992 POTENTIAL.
FT TRANSMEM 993 1010 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1011 1031 POTENTIAL.
FT TRANSMEM 1032 1039 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1040 1060 POTENTIAL.
FT TRANSMEM 1061 1068 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1069 1089 POTENTIAL.
FT TRANSMEM 1090 1099 CYTOPLASMIC (POTENTIAL).
FT REPEAT 494 534 ALPHA-1.
FT REPEAT 979 1010 ALPHA-2.
FT DOMAIN 860 890 POLY-GLU.
FT MOD_RES 658 658 PHOSPHORYLATION (POTENTIAL).
FT CARBOHD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 631 648 MISSING (IN ISOFORM 2).
FT CONFLICT 516 516 V -> I (IN REF. 2).
SQ SEQUENCE 1099 AA: 121374 MW: 3911856BB08B5FD CRC64:
Query Match 6.1%; Score 293; DB 1; Length 1099;
Best Local Similarity 21.7%; Pred. No. 2.4e-11;
Matches 191; Conservative 122; Mismatches 268; Indels 298; Gaps 42:

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Db 614 -LSRRPVAKVMALEDL-----SKPGDAI-----AVDELQDNK---KILKLSPLLT----- 654
QY 368 ILKHAAGQAKKASMSSEVHTDEPEDFISKVF---FDPCSYCLNCGAVILTVYRKGD 424
Db 655 -----RGSSSTSLHNSTIRSTIYQULHSLDP-----LREVR----- 686
QY 425 MSKTYVDYKTEDEGSANAGADYEFTGTVLKPGELOKEFVSIGIIDDFEEDHEFVRL 484
Db 687 LAK-----EKEEESLNGCARQ--PQAKAESR----- 712
QY 465 SNVRIEEDQPEEGMPDPAIFNSLPLPRAVLASPCVATVTIILD--DHAGITFECDTHVS 542
Db 713 -----EEEBPAK-LPAVTVTPAPVP-----DIKGDQKNPG---GQEDVAEA 750
QY 543 ESIGVMEKVLRTSG-----ARGVIVPFRVEGTAGCGGDFPDYTGELFKND---E 593
Db 751 ESTGEMPEGEETAGETEEKSGGETOPEGEGEETOGKGECEDE--NEAGKGDNEGE 809
QY 594 TVKTRVKIVD-----EEEYEROENFIALGEPKMMERGISD--VTDRKLTMEEEKARIA 647
Db 810 DEGEIHAEDGEMKNGEGTESOELSAENHGEAKNDKEGYEDGSGSDGDEEEEBEEO 869
QY 648 EMGKPEVLGEPRLVLEYIIESYEFTKTVDKLIKTNLALVGVTHSWRDQFMEAITYSAGD 707
Db 870 E-----EEEEEEQEEEEEE-----E 885
QY 708 EDEDSGEERLPSCFDY-----VMHFLYFMKVLVACVPPTCYCHMACFAY-----S 755
Db 886 EEEEEKGNDE-PLSLDWPETROKQAIYFLPIVEPMLTVDPVROESRKEFFVTFLOS 944
QY 756 ILITMFLAIIIDLSHSCCTIGLSDYAVAVFVAFGTSVPPTFASKAALQDYVADASI 815
Db 945 IIMIMFSTLWMWMAHXYGETTIGISEETMGLITLLAGSIPPLITSVYARKGL-GDMAY 1003
QY 816 GNVTSNANVNYVLGIGLAMSVAIYWALOGEYHVSAGTAFSVLTFITFAVCISVLY 875
Db 1004 SSSVGSNIFDIVGLPVPPLFLSLNGLOPVVS--SNGFCFAIVLLFLMLFVVISI--- 1059
QY 876 RRRPHLGELGPRCKKATTV-----LFVSLMLYILF 909
Db 1060 -----ASCK--WRMKNILGFTWELLYFVF 1081

RESULT 15
NKX3_MOUSE
ID NKX3_MOUSE STANDARD: PRT: 645 AA.
AC Q99PD7: Q99PD8: Q99JR2:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sodium/potassium/calcium exchanger 3 precursor (Na(+)/K(+)/Ca(2+)-
exchange protein 3).
GN SIC24A3 OR NKX3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ, and CD-1; TISSUE=Embryonic stem cells, and Brain;
RA MEDLINE=21303617; PubMed=11294880;
RA Kraev A., Quekna B.D., Leach S., Li X.-F., Dong H., Winkfein R.,
RA Perizolo M., Cal X., Yang R., Phillips K.D., Lyton J.;
RT "Molecular cloning of a third member of the potassium-dependent
RT sodium-calcium exchanger gene family, NKX3."
RL J. Biol. Chem. 276:23161-23172(2001).
RN [2]
RP SEQUENCE OF 323-645 FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Transports one Ca(2+) and one K(+) in exchange for four
Na(+) (By similarity).

```

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Abundant in the brain. Highest levels found in
CC selected thalamic nuclei, hippocampal CA1 neurons and in layer IV
CC of the cerebral cortex.
CC -1- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC -----
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CC -----
DR EMBL: AF314821; AAG60049.1; -
DR EMBL: AF314822; AAG60050.1; -
DR EMBL: BC005742; AAH05742.1; -
DR MGI: 2137513; SLC24a3.
DR InterPro: IPR004481; K_NaCaexchng.
DR InterPro: IPR004837; NaCa_Exmemb.
DR Pfam: PF01699; Na_Ca_Ex; 3.
DR TRAFRAME: TRGR00367; K_NaCaexchng-rel; 1.
KW Transport; Antiport; Symport; Calcium transport; Potassium transport;
KW Sodium transport; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 43 POTENTIAL.
FT CHAIN 1 44 SODIUM/POTASSIUM/CALCIUM EXCHANGER 3.
FT DOMAIN 44 645 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 107 127 POTENTIAL.
FT DOMAIN 128 151 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 152 172 POTENTIAL.
FT DOMAIN 173 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 202 POTENTIAL.
FT DOMAIN 203 209 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 210 230 POTENTIAL.
FT TRANSMEM 231 234 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 235 255 POTENTIAL.
FT DOMAIN 256 486 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 487 507 POTENTIAL.
FT DOMAIN 508 512 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 513 533 POTENTIAL.
FT DOMAIN 534 551 POTENTIAL.
FT TRANSMEM 552 572 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 573 582 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 583 603 POTENTIAL.
FT DOMAIN 604 617 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 618 638 POTENTIAL.
FT TRANSMEM 639 645 EXTRACELLULAR (POTENTIAL).
FT REPEAT 148 188 ALPHA-1.
FT REPEAT 520 551 ALPHA-2.
FT DOMAIN 424 430 POLY-GLU.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 645 AA; 71914 MW; C62DB6CB4A01C96 CRC64;
SO
Query Match 5.5%; Score 266; DB 1; Length 645;
Best Local Similarity 19.1%; Pred. No. 6.6e-10;
Matches 162; Conservative 94; Mismatches 216; Indels 374; Gaps 30;
QY 77 VIYVFAALIMFGLGVSIADR-FMASIEVITTSQREVTIKKPNGETSTTIRWNEVSN 135
DB 109 VLVHVICAMTFYALAVCDFFVPSLEKICERLH-----LSEDEVAG 150
QY 136 LTLALGSSAPAILLSLIEVCGHGFTA-GDLGSTVGSAAFMFIIGICVYIPDGET 194
DB 151 ATFMAGSSAPDELFTSYIGV-----FITKGVGCTIVGSVFNILCTIGVGLFA--GQV 204
QY 195 RKIKHLRVEFITAAW-----SIFAYIWLWILAVFSPVQVVEGGLTLFFFPVCVLLAW 249
DB 205 VAL-----SSWCLLRDSIYITLSVALYIFIDEKVSWMESLVLYMLIYIYI-- 253
QY 250 VADKRLFFTYMHKRYTDKRGIIITETGDPHKGTBMDGKMANSHFLDGNLVPLEGGKEY 309
DB 254 -----MKYNACIHOCFERTKG-----AGNMYNG--LANN-----AEI 284

QY 310 DESRREMIRILDKLKKHPKEDLDQLEVAMANYALSHQOKSRAFYRIQATRMGTAGNIL 369
DB 285 DDS----- 287
QY 370 KKHAAEQAKKASSNSEVHTDEPEDFISKVFEDPCSYOCLENGCAVLLTVYRKGDMSKTM 429
DB 288 -----SNCDAIV----- 294
QY 430 YVDKTEDGSANAGADVEFEGTVLAKPGTQKEFSGIITDDIFEDDEHFFVRLSNVRI 489
DB 295 -----VLKKANFHKKASVIMDE-----LLSAYPH 320
QY 490 EEEQPEECPMPAIFNSLPLPRAVLASPCVATVTITLDDHAGITFECDTIHVESIGVME 549
DB 321 QLSFSEAGLIMITSHRP-PKTRLS-----MASMLINERRLINSRATYTGSEVAIKIP 375
QY 550 VKVLRISGARGTVIPRTVEGTAKGGGDEDEDYGELEFKNDETVKTIRKIVDEEYEX 609
DB 376 IKHTVENGT-GPSSAPDRGVNGTRR-----DDIVAETD-----NETENE 413
QY 610 KOENFFIALGEPKMERGISDVYDRKLTMEEEAKRAEKGKRVLGEPKLEVIIESEYE 669
DB 414 NEEN-----ENNESD-----EEEE----- 428
QY 670 FKTTVDKLIKTNLALVGVTHSWRDOFMEATVSAAGDEDEDE-----SGE-ERLP 719
DB 429 -----DEDDDGPTTPFPDPGSKLETYK 451
QY 720 SCFDVYMHFTLVFVKVLFACVPTREYCHGV-----ACFAVSILIIIGMLTAIIGDLASHFG 774
DB 452 WAFETWPLSF-----VLXFTVPNCNKP-HWEKFWNTVFASSTILMAFSYMMWVMTIIG 504
QY 775 CTIGLDSVAVVFAVFGTSVPDTPFASKAALODYVADASIGVWTSNANVNLGIGLAW 834
DB 505 YTLGIDPVILGITFLAGTSVPCMASLIYARQGM-GDMAVNSIGSNVFDILIGLPLW 563
QY 835 SVAAI-----YVALOGEPFHVSAAGTLAFSV-----TLTTFIIFAF 867
DB 564 ALDTLANVDYSYIRLNSRGLITSVGLLASVFYTVFVGHVHLNKWQDKKLCGGCLFLXGVE 623
QY 868 VCISVL 873
DB 624 LCFSIM 629

Search completed: November 30, 2002, 12:28:58
Job time : 22.7346 secs